SEQUENCE LISTING

<110> Barnett, Susan
      Zur Megede, Jan

<120> POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
      POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF

<130> PP01631.101

<140> 09/475,704
<141> 1999-12-30

<150> 09/610,313
<151> 2000-07-05

<160> 46

<170> PatentIn Ver. 2.0

<210> 1
<211> 60
<212> DNA
<213> Human immunodeficiency virus

<400> 1
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<210> 2
<211> 60
<212> DNA
<213> Human immunodeficiency virus

<400> 2
gacatccgcc agggccccaa ggagcccttc cgcgactacg tggaccgctt cttcaagacc 60

<210> 3
<211> 1479
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic Gag
      of HIV strain AF110965

<400> 3
atgggcgccc gcgccagcat cctgcgcggc ggcaagctgg acgcctggga gcgcatccgc 60
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ctggagaagt cgccctgaa ccccggcctg ctggagacca gcgagggctg caagcagatc 180
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gacctgaaca cgatgttgaa caccgtgggc ggccaccagg ccgccatgca gatgctgaag 600
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1

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aagcggtgga tcatcctggg cctgaacaag atcgtgcgga tgtacagccc cgtgagcatc 840
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ttcgaggaga ccaccccccgg ccagaagcag gagagcaagg accgcgagac cctgaccagc 1440
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<210> 4
<211> 1509
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic Gag
     of HIV strain AF110967

<400> 4
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ctgcgccccg gcggcaagaa gcactacatg ctgaagcacc tggtgtgggc cagccgcgag 120
ctggagggct cgccctgaa ccccggcctg ctggagaccg ccgagggctg caagcagatc 180
atgaagcagc tgcagcccgc cctgcagacc ggcaccgagg agctgcgcag cctgtacaac 240
accgtggcca ccctgtactg cgtgcacgcc ggcatcgagg tccgcgacac caaggaggcc 300
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caccaggcca tcagcccccg caccctgaac gcctgggtga aggtgatcga ggagaaggcc 480
ttcagccccg aggtgatccc catgttcacc gccctgagcg agggcgccac cccccaggac 540
ctgaacacga tgttgaacac cgtgggcggc caccaggccg ccatgcagat gctgaaggac 600
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gcccccggcc agatgcgcga ccccgcggc agcgacatcg ccggcgccac cagcaccctg 720
caggagcaga tcgcctggat gaccagcaac ccccccgtgc cgtgggcga catctacaag 780
cggtggatca tcctgggcct gaacaagatc gtgcggatgt acagccccgt gagcatcctg 840
gacatccgcc agggccccaa ggagcccttc cgcgactacg tggaccgctt cttcaagacc 900
ctgcgcgccg agcaggccac ccaggacgtg aagaactgga tgaccgagac cctgctggtg 960
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gccgaggcga tgagccaggc caacagcgtg aacatcatga tgcagaagag caacttcaag 1140
ggcccccggc gcaacgtcaa gtgcttcaac tgcggcaagg agggccacat cgccaagaac 1200
tgccgcgccc cccgcaagaa gggctgctgg aagtgcggca aggagggcca ccagatgaag 1260
gactgcaccg agcgccaggc caacttcctg ggcaagatct ggcccagcca aagggccgc 1320
cccggcaact tcctgcagaa ccgcagcgag cccgccgccc ccaccgtgcc caccgccccc 1380
cccgccgaga gcttccgctt cgaggagacc accccggccc ccaagcagga gcccaaggac 1440
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agccagtaa 1509
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<210> 5
<211> 141
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Env common
      region of HIV strain AF110968

<400> 5
accatcacca tcacctgccg catcaagcag atcatcaaca tgtggcagaa ggtgggccgc 60
gccatgtacg cccccccccat cgccggcaac ctgacctgcg agagcaacat caccggcctg 120
ctgctgaccc gcgacggcgg c   141

<210> 6
<211> 1431
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
      gp120 coding region of HIV strain AF110968

<400> 6
agcgtggtgg gcaacctgtg ggtgaccgtg tactacggcg tgcccgtgtg gaaggaggcc 60
aagaccaccc tgttctgcac cagcgacgcc aaggcctacg agaccgaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gcccaccgac cccaaccccc aggagatcgt gctggagaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc tgcgtgaagc tgacccccct gtgcgtgacc 300
ctgaagtgcc gcaacgtgaa cgccaccaac aacatcaaca gcatgatcga acagcagaac 360
aagggcgaga tgaagaactg cagcttcaac gtgaccaccg agctgcgcga ccgcaagcag 420
gaggtgcacg ccctgttcta ccgcctggac gtggtgcccc tgcagggcaa caacagcaac 480
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ttcgacccca tccccatcca ctactgcacc cccgccggct acgccatcct gaagtgcaac 600
aaccagacct tcaacggcac cggcccctgc aacaacgtga gcagcgtgca gtgcgcccac 660
ggcatcaagc ccgtggtgag cacccagctg ctgctgaacg gcagcctggc caagggcgag 720
atcatcatcc gcagcgagaa cctggccaac aacgccaaga tcatcatcgt gcagctgaac 780
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gagcacttca gcaagaaggc catcaagttc gagcccagca gcggcggcga cctggagatc 1020
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gcccccccca tcgccggcaa cctgacctgc gagagcaaca tcaccggcct gctgctgacc 1260
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atgcgcgaca ctggcgcaa cgagctgtac aagtacaagg tggtggagat caagcccctg 1380
ggcgtggccc ccaccgaggc caagcgccgc gtggtggagc gcgagaagcg c   1431

<210> 7
<211> 1944
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
      gp140 coding region of HIV strain AF110968

<400> 7
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aagaccaccc tgttctgcac cagcgacgcc aaggcctacg agaccgaggt gcacaacgtg 120

3

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tgggccaccc acgcctgcgt gcccaccgac cccaacccccc aggagatcgt gctggagaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc tgcgtgaagc tgacccccct gtgcgtgacc 300
ctgaagtgcc gcaacgtgaa cgccaccaac aacatcaaca gcatgatcga caacagcaac 360
aagggcgaga tgaagaactg cagcttcaac gtgaccaccg agctgcgcga ccgcaagcag 420
gaggtgcacg ccctgttcta ccgcctggac gtggtgcccc tgcagggcaa caacagcaac 480
gagtaccgcc tgatcaactg caacaccagc gccatcaccc aggcctgccc caaggtgagc 540
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ggcatcaagc ccgtggtgag cacccagctg ctgctgaacg gcagcctggc caagggcgag 720
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atcaacaact acaccgacac catctaccgc ctgctggagg agagccagaa ccagcaggag 1860
aagaacgaga aggacctgct ggccctggac agctggcaga acctgtggaa ctggttcagc 1920
atcaccaact ggctgtggta catc                                         1944

<210> 8
<211> 2466
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
      gp160 coding region of HIV strain AF110968

<400> 8
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aagaccaccc tgttctgcac cagcgacgcc aaggcctacg agaccgaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gcccaccgac cccaacccccc aggagatcgt gctggagaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
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ctgaagtgcc gcaacgtgaa cgccaccaac aacatcaaca gcatgatcga caacagcaac 360
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gaggtgcacg ccctgttcta ccgcctggac gtggtgcccc tgcagggcaa caacagcaac 480
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ttcgacccca tccccatcca ctactgcacc cccgccggct acgccatcct gaagtgcaac 600
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ggcatcaagc ccgtggtgag cacccagctg ctgctgaacg gcagcctggc caagggcgag 720
atcatcatcc gcagcgagaa cctggccaac aacgccaaga tcatcatcgt gcagctgaac 780
aagcccgtga agatcgtgtg cgtgcgcccc aacaacaaca cccgcaagag cgtgcgcatc 840
ggccccggcc agaccttcta cgccaccggc gagatcatcg cgacatccg ccaggcctac 900
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4

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tgcatcatca acaagaccga gtggaacagc accctgcagg gcgtgagcaa gaagctggag 960
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gcccccccca tcgccggcaa cctgacctgc gagagcaaca tcaccggcct gctgctgacc 1260
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<210> 9
<211> 2547
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
      signal sequence and gp160 coding region of HIV
      strain AF110968

<400> 9
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5
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aagaagagcg ccatcagcct gctggacacc atcgccatcg ccgtggccga gggcaccgac 2460
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cgccagggct cgaggccgc cctgcag                                      2547

<210> 10
<211> 1035
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic a
      gp41 coding region of HIV strain AF110968

<400> 10
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gccgccagca tcaccctgac cgtgcaggcc cgcctgctgc tgagcggcat cgtgcagcag 120
cagaacaacc tgctgcgcgc catcgaggcc cagcagcacc tgctgcagct gaccgtgtgg 180
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gccctgaagt acctgggcag cctggtgcag tactggggcc tggagctgaa gaagagcgcc 900
atcagcctgc tggacaccat cgccatcgcc gtggccgagg caccgaccg catcatcgag 960
ttcatccagc gcatctgccg cgccatccgc aacatcccc gccgcatccg ccaggctc 1020
gaggccgccc tgcag                                                  1035

<210> 11
<211> 144
```

6

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic Env
     common region of HIV strain AF110975

<400> 11
agcatcatca ccctgccctg ccgcatcaag cagatcatcg acatgtggca gaaggtgggc 60
cgcgccatct acgccccccc catcgagggc aacatcacct gcagcagcag catcaccggc 120
ctgctgctgg cccgcgacgg cggc   144

<210> 12
<211> 1437
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
     gp120 coding region of HIV strain AF110975

<400> 12
agcggcctgg gcaacctgtg ggtgaccgtg tacgacggcg tgcccgtgtg cgcgcgaggcc 60
agcaccaccc tgttctgcgc cagcgacgcc aaggcctacg agaaggaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gcccaccgac cccaacccccc aggagatcga gctggacaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc cgcgtgaagc tgacccccct gtgcgtgacc 300
ctgaagtgca ccaactacag caccaactac agcaacacca tgaacgccac cagctacaac 360
aacaacacca ccgaggagat caagaactgc accttcaaca tgaccaccga gctgcgcgac 420
aagaagcagc aggtgtacgc cctgttctac aagctggaca tcgtgcccct gaacagcaac 480
agcagcgagt accgcctgat caactgcaac accagcgcca tcacccaggc ctgccccaag 540
gtgagcttcg accccatccc catccactac tgcgcccccg ccggctacgc catcctgaag 600
tgcaagaaca acaccagcaa cggcaccggc ccctgccaga acgtgagcac cgtgcagtgc 660
acccacggca tcaagcccgt ggtgagcacc cccctgctgc tgaacggcag cctggccgag 720
ggcggcgaga tcatcatccg cagcaagaac ctgagcaaca acgcctacac catcatcgtg 780
cacctgaacg acagcgtgga gatcgtgtgc acccgcccca caacaacac ccgcaagggc 840
atccgcatcg gcccccggcca gaccttctac gccaccgaga acatcatcgg cgacatccgc 900
caggcccact gcaacatcag cgccggcgag tggaacaagg ccgtgcagcg cgtgagcgcc 960
aagctgcgcg agcacttccc caacaagacc atcgagttcc agcccagcag cggcggcgac 1020
ctggagatca ccacccacag cttcaactgc cgcggcgagt cttctactg caacaccagc 1080
aagctgttca acagcagcta caacggcacc agctaccgcg caccgagag caacagcagc 1140
atcatcaccc tgccctgccg catcaagcag atcatcgaca tgtggcagaa ggtgggccgc 1200
gccatctacg cccccccccat cgagggcaac atcacctgca gcagcagcat caccggcctg 1260
ctgctggccc gcgacggcgg cctggacaac atcaccaccg atcttccg ccccccagggc 1320
ggcgacatga aggacaactg cgcgcaacgag ctgtacaagt acaaggtggt ggagatcaag 1380
cccctgggcg tggcccccac cgaggccaag cgccgcgtgg tggagcgcga gaagcgc   1437

<210> 13
<211> 1950
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
     gp140 coding region of HIV strain AF110975

<400> 13

7

```
agcggcctgg gcaacctgtg ggtgaccgtg tacgacggcg tgcccgtgtg gcgcgaggcc 60
agcaccaccc tgttctgcgc cagcgacgcc aaggcctacg agaaggaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gcccaccgac cccaaccccc aggagatcga gctggacaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc cgcgtgaagc tgacccccct gtgcgtgacc 300
ctgaagtgca ccaactacag caccaactac agcaacacca tgaacgccac cagctacaac 360
aacaacacca ccgaggagat caagaactgc accttcaaca tgaccaccga gctgcgcgac 420
aagaagcagc aggtgtacgc cctgttctac aagctggaca tcgtgcccct gaacagcaac 480
agcagcgagt accgcctgat caactgcaac accagcgcca tcacccaggc ctgccccaag 540
gtgagcttcg accccatccc catccactac tgcgcccccg ccggctacgc catcctgaag 600
tgcaagaaca acaccagcaa cggcaccggc ccctgccaga cgtgagcac cgtgcagtgc 660
acccacggca tcaagcccgt ggtgagcacc cccctgctgc tgaacggcag cctggccgag 720
ggcggcgaga tcatcatccg cagcaagaac ctgagcaaca cgcctacac catcatcgtg 780
cacctgaacg acagcgtgga gatcgtgtgc acccgcccca acaacaacac ccgcaagggc 840
atccgcatcg gccccggcca gaccttctac gccaccgaga acatcatcgg cgacatccgc 900
caggcccact gcaacatcag cgccggcgag tggaacaagg ccgtgcagcg cgtgagcgcc 960
aagctgcgcg agcacttccc caacaagacc atcgagttcc agcccagcag cggcggcgac 1020
ctggagatca ccacccacag cttcaactgc cgcggcgagt cttctactg caacaccagc 1080
aagctgttca acagcagcta caacggcacc agctaccgcg gcaccgagag caacagcagc 1140
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gccatctacg ccccccccat cgagggcaac atcacctgca gcagcagcat caccggcctg 1260
ctgctggccc gcgacggcgg cctggacaac atcaccaccg agatcttccg ccccaggc 1320
ggcgacatga aggacaactg cgcgaacgag ctgtacaagt acaaggtggt ggagatcaag 1380
cccctgggcg tggcccccac cgaggccaag cgccgcgtgg tggagcgcga gaagcgcgcc 1440
gtgggcatcg gcgccgtgat cttcggcttc ctgggcgccg ccggcagcaa catgggcgcc 1500
gccagcatca ccctgaccgc ccaggcccgc cagctgctga gcggcatcgt gcagcagcag 1560
agcaacctgc tgcgcgccat cgaggcccag cagcacatgc tgcagctgac cgtgtggggc 1620
atcaagcagc tgcaggcccg cgtgctggcc atcgagcgct acctgaagga ccagcagctg 1680
ctgggcatct ggggctgcag cggcaagctg atctgcacca ccaccgtgcc ctggaacagc 1740
agctggagca acaagaccca gggcgagatc tgggagaaca tgacctggat gcagtgggac 1800
aaggagatca gcaactacac cggcatcatc taccgcctgc tggaggagag ccagaaccag 1860
caggagcaga acgagaagga cctgctggcc ctggacagcc gcaacaacct gtggagctgg 1920
ttcaacatca gcaactggct gtggtacatc                                   1950

<210> 14

<211> 2493
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
      gp160 coding region of HIV strain AF110975

<400> 14
agcggcctgg gcaacctgtg ggtgaccgtg tacgacggcg tgcccgtgtg gcgcgaggcc 60
agcaccaccc tgttctgcgc cagcgacgcc aaggcctacg agaaggaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gcccaccgac cccaaccccc aggagatcga gctggacaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc cgcgtgaagc tgacccccct gtgcgtgacc 300
ctgaagtgca ccaactacag caccaactac agcaacacca tgaacgccac cagctacaac 360
aacaacacca ccgaggagat caagaactgc accttcaaca tgaccaccga gctgcgcgac 420
aagaagcagc aggtgtacgc cctgttctac aagctggaca tcgtgcccct gaacagcaac 480
agcagcgagt accgcctgat caactgcaac accagcgcca tcacccaggc ctgccccaag 540
gtgagcttcg accccatccc catccactac tgcgcccccg ccggctacgc catcctgaag 600
tgcaagaaca acaccagcaa cggcaccggc ccctgccaga cgtgagcac cgtgcagtgc 660
acccacggca tcaagcccgt ggtgagcacc cccctgctgc tgaacggcag cctggccgag 720
```

8

```
ggcggcgaga tcatcatccg cagcaagaac ctgagcaaca acgcctacac catcatcgtg 780
cacctgaacg acagcgtgga gatcgtgtgc acccgcccca acaacaacac ccgcaagggc 840
atccgcatcg gccccggcca gaccttctac gccaccgaga acatcatcgg cgacatccgc 900
caggcccact gcaacatcag cgccggcgag tggaacaagg ccgtgcagcg cgtgagcgcc 960
aagctgcgcg agcacttccc caacaagacc atcgagttcc agcccagcag cggcggcgac 1020
ctggagatca ccacccacag cttcaactgc cgcggcgagt cttctactg caacaccagc 1080
aagctgttca acagcagcta caacggcacc agctaccgcg gcaccgagag caacagcagc 1140
atcatcaccc tgccctgccg catcaagcag atcatcgaca tgtggcagaa ggtgggccgc 1200
gccatctacg cccccccat cgagggcaac atcacctgca gcagcagcat caccggcctg 1260
ctgctggccc gcgacggcgg cctggacaac atcaccaccg agatcttccg cccccagggc 1320
ggcgacatga aggacaactg gcgcaacgag ctgtacaagt acaaggtggt ggagatcaag 1380
cccctggggcg tggccccac cgaggccaag cgccgcgtgg tggagcgcga gaagcgcgcc 1440
gtgggcatcg gcgccgtgat cttcggcttc ctgggcgccg ccggcagcaa catgggcgcc 1500
gccagcatca ccctgaccgc ccaggcccgc cagctgctga gcggcatcgt gcagcagcag 1560
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ctgggcatct ggggctgcag cggcaagctg atctgcacca ccaccgtgcc ctggaacagc 1740
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aaggagatca gcaactacac cggcatcatc taccgcctgc tggaggagag ccagaaccag 1860
caggagcaga cgagaagga cctgctggcc ctggacagcc gcaacaacct gtggagctgg 1920
ttcaacatca gcaactggct gtggtacatc aagatcttca tcatgatcgt gggcggcctg 1980
atcggcctgc gcatcatctt cgccgtgctg agcatcgtga accgcgtgcg ccagggctac 2040
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ctggccctgg cctgggacga cctgcgcagc ctgtgcctgt tcagctacca ccgcctgcgc 2220
gacctgatcc tggtgaccgc ccgcgtggtg gagctgctgg gccgcagcag ccccgcggc 2280
ctgcagcgcg gctgggaggc cctgaagtac ctgggcagcc tggtgcagta ctggggcctg 2340
gagctgaaga gagcgccac cagcctgctg gacagcatcg ccatcgccgt ggccgagggc 2400
accgaccgca tcatcgaggt gatccagcgc atctaccgcg ccttctgcaa catcccccgc 2460
cgcgtgcgcc agggcttcga ggccgccctg cag                            2493

<210> 15
<211> 2565

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
      signal sequence and gp160 coding region of HIV
      strain AF110975

<400> 15
atgcgcgtgc gcggcatcct gcgcagctgg cagcagtggt ggatctgggg catcctgggc 60
ttctggatct gcagcggcct gggcaacctg tgggtgaccg tgtacgacgg cgtgcccgtg 120
tggcgcgagg ccagcaccac cctgttctgc gccagcgacg ccaaggccta cgagaaggag 180
gtgcacaacg tgtgggccac ccacgcctgc gtgcccaccg accccaaccc caggagatc 240
gagctggaca cgtgaccga gaacttcaac atgtggaaga cgacatggt ggaccagatg 300
cacgaggaca tcatcagcct gtgggaccag agcctgaagc ccgcgtgaa gctgaccccc 360
ctgtgcgtga ccctgaagtg caccaactac agcaccaact acagcaacac catgaacgcc 420
accagctaca acaacaacac caccgaggag atcaagaact gcaccttcaa catgaccacc 480
gagctgcgcg acaagaagca gcaggtgtac gccctgttct acaagctgga catcgtgccc 540
ctgaacagca cagcagcga gtaccgcctg atcaactgca caccagcgc catcacccag 600
gcctgccca aggtgagctt cgaccccatc cccatccact actgcgcccc cgccggctac 660
gccatcctga gtgcaagaa caacaccagc aacggcaccg ccccctgcca gaacgtgagc 720
accgtgcagt gcacccacgg catcaagccc gtggtgagca cccccctgct gctgaacggc 780
agcctggccg agggcggcga gatcatcatc cgcagcaaga acctgagcaa caacgcctac 840
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9

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accatcatcg tgcacctgaa cgacagcgtg gagatcgtgt gcacccgccc caacaacaac 900
acccgcaagg gcatccgcat cggcccccggc cagaccttct acgccaccga gaacatcatc 960
ggcgacatcc gccaggccca ctgcaacatc agcgccggcg agtggaacaa ggccgtgcag 1020
cgcgtgagcg ccaagctgcg cgagcacttc cccaacaaga ccatcgagtt ccagcccagc 1080
agcggcggcg acctggagat caccacccac agcttcaact gccgcggcga gttcttctac 1140
tgcaacacca gcaagctgtt caacagcagc tacaacggca ccagctaccg cggcaccgag 1200
agcaacagca gcatcatcac cctgccctgc cgcatcaagc agatcatcga catgtggcag 1260
aaggtgggcc gcgccatcta cgcccccccc atcgagggca acatcacctg cagcagcagc 1320
atcaccggcc tgctgctggc ccgcgacggc ggcctggaca acatcaccac cgagatcttc 1380
cgcccccagg gcggcgacat gaaggacaac tggcgcaacg agctgtacaa gtacaaggtg 1440
gtggagatca agcccctggg cgtggccccc accgaggcca gcgccgcgt ggtggagcgc 1500
gagaagcgcg ccgtgggcat cggcgccgtg atcttcggct cctgggcgc cgccggcagc 1560
aacatgggcg ccgccagcat caccctgacc gcccaggccc gccagctgct gagcggcatc 1620
gtgcagcagc agagcaacct gctgcgcgcc atcgaggccc agcagcacat gctgcagctg 1680
accgtgtggg gcatcaagca gctgcaggcc cgcgtgctgg ccatcgagcg ctacctgaag 1740
gaccagcagc tgctgggcat ctggggctgc agcggcaagc tgatctgcac caccaccgtg 1800
ccctggaaca gcagctggag caacaagacc cagggcgaga tctgggagaa catgacctgg 1860
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ctgtggagct ggttcaacat cagcaactgg ctgtggtaca tcaagatctt catcatgatc 2040
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cgccagggct acagccccct gagcttccag accctgaccc ccaacccccg cggcctggac 2160
cgcctgggcc gcatcgagga ggagggcggc gagcaggacc gcgaccgcag catccgcctg 2220
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caccgcctgc gcgacctgat cctggtgacc gcccgcgtgg tggagctgct gggccgcagc 2340
agcccccgcg gcctgcagcg cggctgggag gccctgaagt acctgggcag cctggtgcag 2400
tactggggcc tggagctgaa gaagagcgcc accagcctgc tggacagcat cgccatcgcc 2460
gtggccgagg gcaccgaccg catcatcgag gtgatccagc gcatctaccg cgccttctgc 2520
aacatccccc gccgcgtgcg ccagggcttc gaggccgccc tgcag            2565


<210> 16

<211> 1056
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic a
      gp41 coding region of HIV strain AF110975

<400> 16
gccgtgggca tcggcgccgt gatcttcggc ttcctgggcg ccgccggcag caacatgggc 60
gccgccagca tcaccctgac cgcccaggcc cgccagctgc tgagcggcat cgtgcagcag 120
cagagcaacc tgctgcgcgc catcgaggcc agcagcaca tgctgcagct gaccgtgtgg 180
ggcatcaagc agctgcaggc ccgcgtgctg gccatcgagc ctacctgaa ggaccagcag 240
ctgctgggca tctggggctg cagcggcaag ctgatctgca ccaccaccgt gccctggaac 300
agcagctgga gcaacaagac ccagggcgag atctgggaga acatgacctg gatgcagtgg 360
gacaaggaga tcagcaacta caccggcatc atctaccgcc tgctggagga gagccagaac 420
cagcaggagc agaacgagaa ggacctgctg gccctggaca gccgcaacaa cctgtggagc 480
tggttcaaca tcagcaactg gctgtggtac atcaagatct tcatcatgat cgtgggcggc 540
ctgatcggcc tgcgcatcat cttcgccgtg ctgagcatcg tgaaccgcgt gcgccaggg c 600
tacagccccc tgagcttcca gaccctgacc cccaacccccc gcggcctgga ccgcctgggc 660
cgcatcgagg aggagggcgg cgagcaggac cgcgaccgca gcatccgcct ggtgcagggc 720
ttcctggccc tggcctggga cgacctgcgc agcctgtgcc tgttcagcta ccaccgcctg 780
cgcgacctga tcctggtgac cgcccgcgtg gtggagctgc tgggccgcag cagcccccgc 840
ggcctgcagc gcggctggga ggccctgaag tacctgggca gcctggtgca gtactggggc 900
ctggagctga agaagagcgc caccagcctg ctggacagca tcgccatcgc cgtggccgag 960
```

10

```
ggcaccgacc gcatcatcga ggtgatccag cgcatctacc gcgccttctg caacatcccc 1020
cgccgcgtgc gccagggctt cgaggccgcc ctgcag                          1056


<210> 17
<211> 492
<212> PRT
<213> Human immunodeficiency virus

<400> 17
Met Gly Ala Arg Ala Ser Ile Leu Arg Gly Gly Lys Leu Asp Ala Trp
 1               5                   10                  15


Glu Arg Ile Arg Leu Arg Pro Gly Gly Lys Lys Cys Tyr Met Met Lys
                20                  25                  30


His Leu Val Trp Ala Ser Arg Glu Leu Glu Lys Phe Ala Leu Asn Pro
            35                  40                  45


Gly Leu Leu Glu Thr Ser Glu Gly Cys Lys Gln Ile Ile Arg Gln Leu
    50                  55                  60


His Pro Ala Leu Gln Thr Gly Ser Glu Glu Leu Lys Ser Leu Phe Asn
65                  70                  75                  80


Thr Val Ala Thr Leu Tyr Cys Val His Glu Lys Ile Glu Val Arg Asp
                85                  90                  95


Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Cys Gln
                100                 105                 110


Gln Lys Ile Gln Gln Ala Glu Ala Ala Asp Lys Gly Lys Val Ser Gln
            115                 120                 125


Asn Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala
    130                 135                 140


Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Ile Glu Glu Lys
145                 150                 155                 160


Ala Phe Ser Pro Glu Val Ile Pro Met Phe Thr Ala Leu Ser Glu Gly
                165                 170                 175


Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His
            180                 185                 190


Gln Ala Ala Met Gln Met Leu Lys Asp Thr Ile Asn Glu Glu Ala Ala
            195                 200                 205


Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly
    210                 215                 220


Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr
225                 230                 235                 240


Leu Gln Glu Gln Ile Ala Trp Met Thr Ser Asn Pro Pro Ile Pro Val
                245                 250                 255
```

```
Gly Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val
        260                 265                 270

Arg Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Lys Gln Gly Pro Lys
        275                 280                 285

Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Phe Lys Thr Leu Arg Ala
    290                 295                 300

Glu Gln Ser Thr Gln Glu Val Lys Asn Trp Met Thr Asp Thr Leu Leu
305                 310                 315                 320

Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Arg Ala Leu Gly
            325                 330                 335

Pro Gly Ala Ser Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly
            340                 345                 350

Gly Pro Ser His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Ala
        355                 360                 365

Asn Thr Ser Val Met Met Gln Lys Ser Asn Phe Lys Gly Pro Arg Arg
    370                 375                 380

Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Arg Asn
385                 390                 395                 400

Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly
            405                 410                 415

His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys
            420                 425                 430

Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Ser Arg
        435                 440                 445

Pro Glu Pro Thr Ala Pro Pro Ala Glu Ser Phe Arg Phe Glu Glu Thr
    450                 455                 460

Thr Pro Gly Gln Lys Gln Glu Ser Lys Asp Arg Glu Thr Leu Thr Ser
465                 470                 475                 480

Leu Lys Ser Leu Phe Gly Asn Asp Pro Leu Ser Gln
            485                 490


<210> 18
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
      signal sequence of HIV strain AF110968

<400> 18
```

```
atgcgcgtga tgggcatcct gaagaactac cagcagtggt ggatgtgggg catcctgggc 60
ttctggatgc tgatcatcag c                                          81

<210> 19
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
      signal sequence of HIV strain AF110975

<400> 19
atgcgcgtgc gcggcatcct gcgcagctgg cagcagtggt ggatctgggg catcctgggc 60
ttctggatct gc                                                    72

<210> 20
<211> 1479
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic Gag
      coding sequence of HIV strain AF110965


<400> 20
atgggcgccc gcgccagcat cctgcgcggc ggcaagctgg acgcctggga gcgcatccgc 60
ctgcgccccg gcggcaagaa gtgctacatg atgaagcacc tggtgtgggc cagccgcgag 120
ctggagaagt cgccctgaa ccccggcctg ctggagacca gcgagggctg caagcagatc 180
atccgccagc tgcaccccgc cctgcagacc ggcagcgagg agctgaagag cctgttcaac 240
accgtggcca ccctgtactg cgtgcacgag aagatcgagg tgcgcgacac caaggaggcc 300
ctggacaaga tcgaggagga gcagaacaag tgccagcaga gatccagca ggccgaggcc 360
gccgacaagg gcaaggtgag ccagaactac cccatcgtgc agaacctgca gggccagatg 420
gtgcaccagg ccatcagccc ccgcaccctg aacgcctggg tgaaggtgat cgaggagaag 480
gccttcagcc ccgaggtgat ccccatgttc accgccctga gcgagggcgc cacccccag 540
gacctgaaca ccatgctgaa caccgtgggc ggccaccagg ccgccatgca gatgctgaag 600
gacaccatca cgaggaggc cgccgagtgg gaccgcgtgc accccgtgca cgccggcccc 660
atcgccccg gccagatgcg cgagccccgc ggcagcgaca tcgccggcac caccagcacc 720
ctgcaggagc agatcgcctg gatgaccagc aaccccccca tccccgtggg cgacatctac 780
aagcgctgga tcatcctggg cctgaacaag atcgtgcgca tgtacagccc cgtgagcatc 840
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accctgcgcg ccgagcagag cacccaggag gtgaagaact ggatgaccga caccctgctg 960
gtgcagaacg ccaaccccga ctgcaagacc atcctgcgcg ccctgggccc cggcgccagc 1020
ctggaggaga tgatgaccgc ctgccagggc gtgggcggcc ccagccacaa ggcccgcgtg 1080
ctggccgagg ccatgagcca ggccaacacc agcgtgatga tgcagaagag caacttcaag 1140
ggcccccgcc gcatcgtgaa gtgcttcaac tgcggcaagg agggccacat cgcccgcaac 1200
tgccgcgccc cccgcaagaa gggctgctgg aagtgcggca aggagggcca ccagatgaag 1260
gactgcaccg agcgccaggc caacttcctg ggcaagatct ggcccagcca aagggccgc 1320
cccggcaact tcctgcagag ccgccccgag cccaccgccc ccccgccga gagcttccgc 1380
ttcgaggaga ccaccccgg ccagaagcag gagagcaagg accgcgagac cctgaccagc 1440
ctgaagagcc tgttcggcaa cgaccccctg agccagtaa                        1479

<210> 21
<211> 1509
<212> DNA
<213> Artificial Sequence
```

13

<220>
<223> Description of Artificial Sequence: synthetic Gag
      coding sequence of HIV strain AF110967

<400> 21
atgggcgccc gcgccagcat cctgcgcggc gagaagctgg acaagtggga gaagatccgc 60
ctgcgccccg gcggcaagaa gcactacatg ctgaagcacc tggtgtgggc cagccgcgag 120
ctggagggct cgccctgaa ccccggcctg ctggagaccg ccgagggctg caagcagatc 180
atgaagcagc tgcagcccgc cctgcagacc ggcaccgagg agctgcgcag cctgtacaac 240
accgtggcca ccctgtactg cgtgcacgcc ggcatcgagg tgcgcgacac caaggaggcc 300
ctggacaaga tcgaggagga gcagaacaag agccagcaga gacccagca ggccaaggag 360
gccgacggca aggtgagcca gaactacccc atcgtgcaga acctgcaggg ccagatggtg 420
caccaggcca tcagcccccg caccctgaac gcctgggtga aggtgatcga ggagaaggcc 480
ttcagccccg aggtgatccc catgttcacc gccctgagcg agggcgccac cccccaggac 540
ctgaacacca tgctgaacac cgtgggcggc caccaggccg ccatgcagat gctgaaggac 600
accatcaacg aggaggccgc cgagtgggac cgcctgcacc ccgtgcaggc cggccccgtg 660
gcccccggcc agatgcgcga cccccgcggc agcgacatcg ccggcgccac cagcaccctg 720
caggagcaga tcgcctggat gaccagcaac ccccccgtgc ccgtgggcga catctacaag 780
cgctggatca tcctgggcct gaacaagatc gtgcgcatgt acagccccgt gagcatcctg 840
gacatccgcc agggccccaa ggagcccttc cgcgactacg tggaccgctt cttcaagacc 900
ctgcgcgccg agcaggccac ccaggacgtg aagaactgga tgaccgagac cctgctggtg 960
cagaacgcca accccgactg caagaccatc ctgcgcgccc tgggcccccgg cgccaccctg 1020
gaggagatga tgaccgcctg ccagggcgtg ggcggccccg gccacaaggc ccgcgtgctg 1080
gccgaggcca tgagccaggc caacagcgtg aacatcatga tgcagaagag caacttcaag 1140
ggccccccgcc gcaacgtgaa gtgcttcaac tgcggcaagg agggccacat cgccaagaac 1200
tgccgcgccc cccgcaagaa gggctgctgg aagtgcggca aggagggcca ccagatgaag 1260
gactgcaccg agcgccaggc caacttcctg ggcaagatct ggcccagcca aagggccgc 1320
cccggcaact tcctgcagaa ccgcagcgag cccgccgccc ccaccgtgcc caccgcccccc 1380
cccgccgaga gcttccgctt cgaggagacc accccccgccc ccaagcagga gcccaaggac 1440
cgcgagccct accgcgagcc cctgaccgcc ctgcgcagcc tgttcggcag cggccccctg 1500
agccagtaa   1509

<210> 22
<211> 502
<212> PRT
<213> Human immunodeficiency virus

<400> 22
Met Gly Ala Arg Ala Ser Ile Leu Arg Gly Glu Lys Leu Asp Lys Trp
  1   5   10   15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys His Tyr Met Leu Lys
               20   25   30

His Leu Val Trp Ala Ser Arg Glu Leu Glu Gly Phe Ala Leu Asn Pro
          35   40   45

Gly Leu Leu Glu Thr Ala Glu Gly Cys Lys Gln Ile Met Lys Gln Leu
     50   55   60

Gln Pro Ala Leu Gln Thr Gly Thr Glu Glu Leu Arg Ser Leu Tyr Asn
 65   70   75   80

Thr Val Ala Thr Leu Tyr Cys Val His Ala Gly Ile Glu Val Arg Asp
               85   90   95

14

```
Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Gln
        100                 105                 110

Gln Lys Thr Gln Gln Ala Lys Glu Ala Asp Gly Lys Val Ser Gln Asn
        115                 120                 125

Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala Ile
        130                 135                 140

Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Ile Glu Glu Lys Ala
145                 150                 155                 160

Phe Ser Pro Glu Val Ile Pro Met Phe Thr Ala Leu Ser Glu Gly Ala
                165                 170                 175

Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
        180                 185                 190

Ala Ala Met Gln Met Leu Lys Asp Thr Ile Asn Glu Glu Ala Ala Glu
        195                 200                 205

Trp Asp Arg Leu His Pro Val Gln Ala Gly Pro Val Ala Pro Gly Gln
210                 215                 220

Met Arg Asp Pro Arg Gly Ser Asp Ile Ala Gly Ala Thr Ser Thr Leu
225                 230                 235                 240

Gln Glu Gln Ile Ala Trp Met Thr Ser Asn Pro Pro Val Pro Val Gly
                245                 250                 255

Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
                260                 265                 270

Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
        275                 280                 285

Pro Phe Arg Asp Tyr Val Asp Arg Phe Phe Lys Thr Leu Arg Ala Glu
        290                 295                 300

Gln Ala Thr Gln Asp Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
305                 310                 315                 320

Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Arg Ala Leu Gly Pro
                325                 330                 335

Gly Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
        340                 345                 350

Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Ala Asn
        355                 360                 365

Ser Val Asn Ile Met Met Gln Lys Ser Asn Phe Lys Gly Pro Arg Arg
        370                 375                 380

Asn Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Lys Asn
385                 390                 395                 400
```

15

```
Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly
            405             410             415

His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys
            420             425             430

Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Asn Arg
            435             440             445

Ser Glu Pro Ala Ala Pro Thr Val Pro Thr Ala Pro Pro Ala Glu Ser
    450             455             460

Phe Arg Phe Glu Glu Thr Thr Pro Ala Pro Lys Gln Glu Pro Lys Asp
465             470             475             480

Arg Glu Pro Tyr Arg Glu Pro Leu Thr Ala Leu Arg Ser Leu Phe Gly
            485             490             495


Ser Gly Pro Leu Ser Gln
            500
```

<210> 23
<211> 849
<212> PRT
<213> Human immunodeficiency virus

<400> 23
```
Met Arg Val Met Gly Ile Leu Lys Asn Tyr Gln Gln Trp Trp Met Trp
  1             5             10             15

Gly Ile Leu Gly Phe Trp Met Leu Ile Ile Ser Ser Val Val Gly Asn
            20             25             30

Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Lys
            35             40             45

Thr Thr Leu Phe Cys Thr Ser Asp Ala Lys Ala Tyr Glu Thr Glu Val
    50             55             60

His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
65             70             75             80

Gln Glu Ile Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys
            85             90             95

Asn Asp Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
            100             105             110

Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
            115             120             125

Lys Cys Arg Asn Val Asn Ala Thr Asn Asn Ile Asn Ser Met Ile Asp
            130             135             140

Asn Ser Asn Lys Gly Glu Met Lys Asn Cys Ser Phe Asn Val Thr Thr
```

Glu Leu Arg Asp Arg Lys Gln Glu Val His Ala Leu Phe Tyr Arg Leu
                165   170   175

Asp Val Val Pro Leu Gln Gly Asn Asn Ser Asn Glu Tyr Arg Leu Ile
                180   185   190

Asn Cys Asn Thr Ser Ala Ile Thr Gln Ala Cys Pro Lys Val Ser Phe
        195   200   205

Asp Pro Ile Pro Ile His Tyr Cys Thr Pro Ala Gly Tyr Ala Ile Leu
        210   215   220

Lys Cys Asn Asn Gln Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val
225   230   235   240

Ser Ser Val Gln Cys Ala His Gly Ile Lys Pro Val Val Ser Thr Gln
                245   250   255

Leu Leu Leu Asn Gly Ser Leu Ala Lys Gly Glu Ile Ile Ile Arg Ser
                260   265   270

Glu Asn Leu Ala Asn Asn Ala Lys Ile Ile Ile Val Gln Leu Asn Lys
        275   280   285

Pro Val Lys Ile Val Cys Val Arg Pro Asn Asn Asn Thr Arg Lys Ser
        290   295   300

Val Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Glu Ile Ile
305   310   315   320

Gly Asp Ile Arg Gln Ala Tyr Cys Ile Ile Asn Lys Thr Glu Trp Asn
                325   330   335

Ser Thr Leu Gln Gly Val Ser Lys Lys Leu Glu Glu His Phe Ser Lys
                340   345   350

Lys Ala Ile Lys Phe Glu Pro Ser Ser Gly Gly Asp Leu Glu Ile Thr
        355   360   365

Thr His Ser Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asp Thr Ser
        370   375   380

Gln Leu Phe Asn Ser Thr Tyr Ser Pro Ser Phe Asn Gly Thr Glu Asn
385   390   395   400

Lys Leu Asn Gly Thr Ile Thr Ile Thr Cys Arg Ile Lys Gln Ile Ile
                405   410   415

Asn Met Trp Gln Lys Val Gly Arg Ala Met Tyr Ala Pro Pro Ile Ala
                420   425   430

Gly Asn Leu Thr Cys Glu Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg
        435   440   445

Asp Gly Gly Lys Thr Gly Pro Asn Asp Thr Glu Ile Phe Arg Pro Gly

17

```
              450                    455                    460

Gly Gly Asp Met Arg Asp Asn Trp Arg Asn Glu Leu Tyr Lys Tyr Lys
465                 470                 475                 480

Val Val Glu Ile Lys Pro Leu Gly Val Ala Pro Thr Glu Ala Lys Arg
                485                 490                 495

Arg Val Val Glu Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Val Phe
            500                 505                 510

Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Ile
        515                 520                 525


Thr Leu Thr Val Gln Ala Arg Leu Leu Leu Ser Gly Ile Val Gln Gln
        530                 535                 540

Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln
545                 550                 555                 560

Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Thr Arg Ile Leu Ala Val
                565                 570                 575

Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser
            580                 585                 590

Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ser Ser Trp Ser
            595                 600                 605

Asn Arg Ser His Asp Glu Ile Trp Asp Asn Met Thr Trp Met Gln Trp
            610                 615                 620

Asp Arg Glu Ile Asn Asn Tyr Thr Asp Thr Ile Tyr Arg Leu Leu Glu
625                 630                 635                 640

Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Lys Asp Leu Leu Ala Leu
                645                 650                 655

Asp Ser Trp Gln Asn Leu Trp Asn Trp Phe Ser Ile Thr Asn Trp Leu
            660                 665                 670

Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu
            675                 680                 685

Arg Ile Ile Phe Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly
        690                 695                 700

Tyr Ser Pro Leu Pro Phe Gln Thr Leu Thr Pro Asn Pro Arg Glu Pro
705                 710                 715                 720

Asp Arg Leu Gly Arg Ile Glu Glu Glu Gly Gly Glu Gln Asp Arg Gly
                725                 730                 735

Arg Ser Ile Arg Leu Val Ser Gly Phe Leu Ala Leu Ala Trp Asp Asp
            740                 745                 750
```

18

```
Leu Arg Ser Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Phe Ile
    755                 760             765

Leu Ile Ala Ala Arg Val Leu Glu Leu Leu Gly Gln Arg Gly Trp Glu
    770             775             780

Ala Leu Lys Tyr Leu Gly Ser Leu Val Gln Tyr Trp Gly Leu Glu Leu
785             790             795             800

Lys Lys Ser Ala Ile Ser Leu Leu Asp Thr Ile Ala Ile Ala Val Ala
            805             810             815


Glu Gly Thr Asp Arg Ile Ile Glu Phe Ile Gln Arg Ile Cys Arg Ala
        820             825             830

Ile Arg Asn Ile Pro Arg Arg Ile Arg Gln Gly Phe Glu Ala Ala Leu
    835             840             845

Gln


<210> 24
<211> 855
<212> PRT
<213> Human immunodeficiency virus

<400> 24
Met Arg Val Arg Gly Ile Leu Arg Ser Trp Gln Gln Trp Trp Ile Trp
  1             5               10              15

Gly Ile Leu Gly Phe Trp Ile Cys Ser Gly Leu Gly Asn Leu Trp Val
            20              25              30

Thr Val Tyr Asp Gly Val Pro Val Trp Arg Glu Ala Ser Thr Thr Leu
        35              40              45

Phe Cys Ala Ser Asp Ala Lys Ala Tyr Glu Lys Glu Val His Asn Val
    50              55              60

Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Ile
65              70              75              80

Glu Leu Asp Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asp Met
            85              90              95

Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
            100             105             110

Lys Pro Arg Val Lys Leu Thr Pro Leu Cys Val Thr Leu Lys Cys Thr
        115             120             125

Asn Tyr Ser Thr Asn Tyr Ser Asn Thr Met Asn Ala Thr Ser Tyr Asn
    130             135             140

Asn Asn Thr Thr Glu Glu Ile Lys Asn Cys Thr Phe Asn Met Thr Thr
```

19

Glu Leu Arg Asp Lys Lys Gln Gln Val Tyr Ala Leu Phe Tyr Lys Leu
            165   170   175

Asp Ile Val Pro Leu Asn Ser Asn Ser Ser Glu Tyr Arg Leu Ile Asn
            180   185   190

Cys Asn Thr Ser Ala Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Asp
            195   200   205

Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys
    210   215   220

Cys Lys Asn Asn Thr Ser Asn Gly Thr Gly Pro Cys Gln Asn Val Ser
225   230   235   240

Thr Val Gln Cys Thr His Gly Ile Lys Pro Val Val Ser Thr Pro Leu
            245   250   255

Leu Leu Asn Gly Ser Leu Ala Glu Gly Gly Glu Ile Ile Ile Arg Ser
            260   265   270

Lys Asn Leu Ser Asn Asn Ala Tyr Thr Ile Ile Val His Leu Asn Asp
            275   280   285

Ser Val Glu Ile Val Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly
    290   295   300

Ile Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Glu Asn Ile Ile
305   310   315   320

Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Ala Gly Glu Trp Asn
            325   330   335

Lys Ala Val Gln Arg Val Ser Ala Lys Leu Arg Glu His Phe Pro Asn
            340   345   350

Lys Thr Ile Glu Phe Gln Pro Ser Ser Gly Gly Asp Leu Glu Ile Thr
            355   360   365

Thr His Ser Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asn Thr Ser
    370   375   380

Lys Leu Phe Asn Ser Ser Tyr Asn Gly Thr Ser Tyr Arg Gly Thr Glu
385   390   395   400

Ser Asn Ser Ser Ile Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile
            405   410   415

Asp Met Trp Gln Lys Val Gly Arg Ala Ile Tyr Ala Pro Pro Ile Glu
            420   425   430

Gly Asn Ile Thr Cys Ser Ser Ser Ile Thr Gly Leu Leu Leu Ala Arg
            435   440   445

Asp Gly Gly Leu Asp Asn Ile Thr Thr Glu Ile Phe Arg Pro Gln Gly

20

```
            450                    455                    460

Gly Asp Met Lys Asp Asn Trp Arg Asn Glu Leu Tyr Lys Tyr Lys Val
465                470                475                480

Val Glu Ile Lys Pro Leu Gly Val Ala Pro Thr Glu Ala Lys Arg Arg
                485                490                495

Val Val Glu Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Val Ile Phe
                500                505                510

Gly Phe Leu Gly Ala Ala Gly Ser Asn Met Gly Ala Ala Ser Ile Thr
            515                520                525

Leu Thr Ala Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln
    530                535                540

Ser Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Met Leu Gln Leu
545                550                555                560

Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Val Leu Ala Ile Glu
            565                570                575

Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly
            580                585                590

Lys Leu Ile Cys Thr Thr Thr Val Pro Trp Asn Ser Ser Trp Ser Asn
            595                600                605

Lys Thr Gln Gly Glu Ile Trp Glu Asn Met Thr Trp Met Gln Trp Asp
    610                615                620

Lys Glu Ile Ser Asn Tyr Thr Gly Ile Ile Tyr Arg Leu Leu Glu Glu
625                630                635                640

Ser Gln Asn Gln Gln Glu Gln Asn Glu Lys Asp Leu Leu Ala Leu Asp
            645                650                655

Ser Arg Asn Asn Leu Trp Ser Trp Phe Asn Ile Ser Asn Trp Leu Trp
            660                665                670

Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu Arg
            675                680                685

Ile Ile Phe Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr
    690                695                700

Ser Pro Leu Ser Phe Gln Thr Leu Thr Pro Asn Pro Arg Gly Leu Asp
705                710                715                720

Arg Leu Gly Arg Ile Glu Glu Glu Gly Gly Glu Gln Asp Arg Asp Arg
            725                730                735

Ser Ile Arg Leu Val Gln Gly Phe Leu Ala Leu Ala Trp Asp Asp Leu
            740                745                750
```

21

```
Arg Ser Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Ile Leu
    755                 760                 765

Val Thr Ala Arg Val Val Glu Leu Leu Gly Arg Ser Ser Pro Arg Gly
    770             775                 780

Leu Gln Arg Gly Trp Glu Ala Leu Lys Tyr Leu Gly Ser Leu Val Gln
785                 790                 795                 800

Tyr Trp Gly Leu Glu Leu Lys Lys Ser Ala Thr Ser Leu Leu Asp Ser
            805                 810                 815

Ile Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Ile Ile Glu Val Ile
            820                 825                 830

Gln Arg Ile Tyr Arg Ala Phe Cys Asn Ile Pro Arg Arg Val Arg Gln
    835                 840                 845

Gly Phe Glu Ala Ala Leu Gln
    850             855


<210> 25
<211> 20
<212> PRT
<213> Human immunodeficiency virus

<400> 25
Asp Ile Lys Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg
  1             5                 10                 15

Phe Phe Lys Thr
            20


<210> 26
<211> 60
<212> DNA
<213> Human immunodeficiency virus

<400> 26
gacataaaac aaggaccaaa agagcccttt agagactatg tagaccggtt ctttaaaacc 60

<210> 27
<211> 20
<212> PRT
<213> Human immunodeficiency virus

<400> 27
Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg
  1             5                 10                 15

Phe Phe Lys Thr
            20
```

<210> 28
<211> 47
<212> PRT
<213> Human immunodeficiency virus

<400> 28
Thr Ile Thr Ile Thr Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln
 1   5   10   15

Lys Val Gly Arg Ala Met Tyr Ala Pro Pro Ile Ala Gly Asn Leu Thr
                20   25   30

Cys Glu Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
            35   40   45

<210> 29
<211> 48
<212> PRT
<213> Human immunodeficiency virus

<400> 29
Ser Ile Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asp Met Trp
 1   5   10   15

Gln Lys Val Gly Arg Ala Ile Tyr Ala Pro Pro Ile Glu Gly Asn Ile
                20   25   30

Thr Cys Ser Ser Ser Ile Thr Gly Leu Leu Leu Ala Arg Asp Gly Gly
            35   40   45

<210> 30
<211> 2469
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PR975(+)

<400> 30
gtcgacgcca ccatggccga ggccatgagc caggccacca gcgccaacat cctgatgcag 60
cgcagcaact tcaagggccc caagcgcatc atcaagtgct tcaactgcgg caaggagggc 120
cacatcgccc gcaactgccg cgccccccgc aagaagggct gctggaagtg cggcaaggag 180
ggccaccaga tgaaggactg caccgagcgc caggccaact tcttccgcga ggacctggcc 240
ttcccccagg gcaaggcccg cgagttcccc agcgagcaga accgcgccaa cagccccacc 300
agccgcgagc tgcaggtgcg cggcgacaac ccccgcagcg aggccggcgc cgagcgccag 360
ggcaccctga acttccccca gatcaccctg tggcagcgcc ccctggtgag catcaaggtg 420
ggcggccaga tcaaggaggc cctgctggac accggcgccg acgacaccgt gctggaggag 480
atgagcctgc ccggcaagtg gaagcccaag atgatcggcg gcatcggcgg cttcatcaag 540
gtgcgccagt acgaccagat cctgatcgag atctgcggca gaaggccat cggcaccgtg 600
ctgatcggcc ccacccccgt gaacatcatc ggccgcaaca tgctgaccca gctgggctgc 660
accctgaact tccccatcag ccccatcgag accgtgcccg tgaagctgaa gcccggcatg 720
gacggcccca aggtgaagca gtggcccctg accgaggaga agatcaaggc cctgaccgcc 780
atctgcgagg agatggagaa ggagggcaag atcaccaaga tcggccccga gaaccccta c 840
aacaccccccg tgttcgccat caagaagaag gacagcacca agtggcgcaa gctggtggac 900
ttccgcgagc tgaacaagcg cacccaggac ttctgggagg tgcagctggg catcccccac 960

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cccgccggcc tgaagaagaa gaagagcgtg accgtgctgg acgtgggcga cgcctacttc 1020
agcgtgcccc tggacgagga cttccgcaag tacaccgcct tcaccatccc cagcatcaac 1080
aacgagaccc ccggcatccg ctaccagtac aacgtgctgc cccagggctg gaagggcagc 1140
cccagcatct tccagagcag catgaccaag atcctggagc ccttccgcgc ccgcaacccc 1200
gagatcgtga tctaccagta catggacgac ctgtacgtgg gcagcgacct ggagatcggc 1260
cagcaccgcg ccaagatcga ggagctgcgc aagcacctgc tgcgctgggg cttcaccacc 1320
cccgacaaga agcaccagaa ggagccccccc ttcctgtgga tgggctacga gctgcacccc 1380
gacaagtgga ccgtgcagcc catcgagctg cccgagaagg agagctggac cgtgaacgac 1440
atccagaagc tggtgggcaa gctgaactgg gccagccaga tctaccccgg catcaaggtg 1500
cgccagctgt gcaagctgct gcgcggcgcc aaggccctga ccgacatcgt gcccctgacc 1560
gaggaggccg agctggagct ggccgagaac cgcgagatcc tgcgcgagcc cgtgcacggc 1620
gtgtactacg accccagcaa ggacctggtg gccgagatcc agaagcaggg ccacgaccag 1680
tggacctacc agatctacca ggagcccttc aagaacctga agaccggcaa gtacgccaag 1740
atgcgcaccg cccacaccaa cgacgtgaag cagctgaccg aggccgtgca gaagatcgcc 1800
atggagagca tcgtgatctg gggcaagacc cccaagttcc gcctgcccat ccagaaggag 1860
acctgggaga cctggtggac cgactactgg caggccacct ggatccccga gtgggagttc 1920
gtgaacaccc ccccccctggt gaagctgtgg taccagctgg agaaggagcc catcatcggc 1980
gccgagacct tctacgtgga cggcgccgcc aaccgcgaga ccaagatcgg caaggccggc 2040
tacgtgaccg accggggccg gcagaagatc gtgagcctga ccgagaccac caaccagaag 2100
accgagctgc aggccatcca gctggccctg caggacagcg gcagcgaggt gaacatcgtg 2160
accgacagcc agtacgccct gggcatcatc caggcccagc ccgacaagag cgagagcgag 2220
ctggtgaacc agatcatcga gcagctgatc aagaaggaga aggtgtacct gagctgggtg 2280
cccgcccaca agggcatcgg cggcaacgag cagatcgaca agctggtgag caagggcatc 2340
cgcaaggtgc tgttcctgga cggcatcgat ggcggcatcg tgatctacca gtacatggac 2400
gacctgtacg tgggcagcgg cggcccctagg atcgattaaa agcttcccgg ggctagcacc 2460
ggtgaattc                                                          2469

<210> 31
<211> 2463
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PR975YM

<400> 31
gtcgacgcca ccatggccga ggccatgagc caggccacca gcgccaacat cctgatgcag 60
cgcagcaact tcaagggccc caagcgcatc atcaagtgct tcaactgcgg caaggagggc 120
cacatcgccc gcaactgccg cgcccccccgc aagaagggct gctggaagtg cggcaaggag 180
ggccaccaga tgaaggactg caccgagcgc caggccaact tcttccgcga ggacctggcc 240
ttcccccagg gcaaggcccg cgagttcccc agcgagcaga accgcgccaa cagccccacc 300
agccgcgagc tgcaggtgcg cggcgacaac ccccgcagcg aggccggcgc cgagcgccag 360
ggcacccctga acttcccccca gatcaccctg tggcagcgcc ccctggtgag catcaaggtg 420
ggcggccaga tcaaggaggc cctgctggac accggcgccg acgacaccgt gctggaggag 480
atgagcctgc ccggcaagtg gaagcccaag atgatcggcg gcatcggcgg cttcatcaag 540
gtgcgccagt acgaccagat cctgatcgag atctgcggca agaaggccat cggcaccgtg 600
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<212> DNA
<213> Human immunodeficiency virus

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<212> DNA
<213> Human immunodeficiency virus

<400> 35
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29

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<212> DNA
<213> Human immunodeficiency virus


<400> 36
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<210> 37
<211> 18
<212> PRT
<213> Human immunodeficiency virus


<400> 37
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Gly Gly




<210> 38
<211> 38
<212> DNA
<213> Artificial Sequence


<220>
<223> Description of Artificial Sequence: primer
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<400> 38
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<210> 39
<211> 38
<212> DNA
<213> Artificial Sequence


<220>
<223> Description of Artificial Sequence: primer
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<400> 39
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<212> DNA
<213> Artificial Sequence

<220>
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<210> 41
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer
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<210> 42
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<212> DNA
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<220>
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<210> 43
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<212> DNA
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<223> Description of Artificial Sequence: primer
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<212> DNA
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<213> Human immunodeficiency virus

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32

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33

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34

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<220>
<223> Description of Artificial Sequence: spacer

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